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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. ŏ . is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

AUTHORS	REFERENCE	VERSION KEYWORDS SOURCE ORGANISM	ACCESSION	RESULT 1 HSA534331 LOCUS		45	0 C 44		C 40		37	ω. π.	3 3 n 4	ມູນ	31	c 29	C 28	c 26 27			22		19	17 18	16		13		_	p 00	7 5		نا حاس		_ :	, X	
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necher,H. and Renauld,J.C.	Vertebrata; Euteleostomi; l; Hominidae; Homo.	ne Receptor	Likely Interleukin or			Mus mus	AC121152 Mus muscu AC134351 Rattus no	AC143800 Macaca mu	Rattu	AC020907 Homo sapi	AB058686 Homo sapi		98 Omo	AC127778 Rattus no	ACO96180 Rattus no	AC099283 Rattus no	AC103435 Rattus no		lomo sar	AX070806 Sequence	equenc	AC123354 Rattue no	AL662911 Mouse DNA	AX478525 Sequence	AX497167 Sequence		AY184376 Mus muscu		AL590683 Human DNA		AX129152 Homo sapi AX478497 Sequence	29151 Homo	AX478514 Sequence	534330 Homo	AJS34331 Homo sand	-	

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Submitted (06-DEC-2002) Renauld J.C., UCL for Cancer Research, 74 Avenue Hippocrate,
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(LICR2 gene) .
AJ534330 1 GI:26986037
LICR3 gene; Likely Interleukin or Cy
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547 CCAGTCCAGATCACTCTCCAGCCAGCTGCCAGCGAACACCACTGCCTCAGTGCCAGAACC 606	ą	Direct Submission	TITLE
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421 GCCAATGCCACGTACCAGCTGCCCCCTGCATGCCCCCACTGGATCTGAAGTATGAGGTG 480	Db	Mammalia; Eutheria; Primates;	REFERENCE
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/note="alternatively spliced" /codon_start=1 /produce="alternatively spliced" /produce="alterlawkin 28 receptor A" /protein_id="AAN28266.1" /protein_id="AAN28266.1" /db_xref="G1:25527122" /db_xref="G1:25527122" /translation="MAGPERWEPLLICLLQAAPGRPRLAPPQNVTLLSQNFSVYLTWL PGLGNPQDVTYFVAYQSSPTRRWREVEECAGTKELLCSMMCLKXQDLYNKFKGRVRT VSPSSKSPWYESEYLDYLFEVESPAPPVLVLTQTEEILSANATTYTFSVPKYSKFSKPTCF AFWKEGAGNKTLFPVTPHGQPVQITLQPAASEHHCLSARTTYTFSVPKYSKFSKPTCF	/note="synonym: zcytor19" 1. 1563 /genpamily8RA"	<u> </u>	Location/Qualifiers 1. 1563 /organism="Homo sapiens"	and Grant, F. J.  and Grant, F. J.  Direct Submission  Submitted (05-JUL-2002) Bioinformatics, 2  Eartlab A. 100-101-101-101-101-101-101-101-101-101	and Grant, F.J. IL28RA Unpublished 2 (bases 1 to 1563)	Eukar Mamma 1 (b Shepp	3	AY129151  1563 bp mRNA linear PRI 26-NOV-2002  NH Homo sapiens interleukin 28 receptor A (IL28RA) mRNA, complete cds; alternatively spliced.  AY129151		1436 AGGTGA 1441        1558 AGGTGA 1563	1376 GGGGCTGAGAGCACCCAGAGGACCCGAGGACACTGGGCCCGGACATTACATGGCC 1435	1316 CCTGAGGAGGAAGGAGGCGAGGGAATCAGAAATTGAGGACAGCGATGCGGGCAGCTGG 1375	1256 CTGGTCCCTGGGGGACCCCCAGTTTCTCTTCAGACACTGACCTTCTGCTGGGAAAGCAGC 1315 -	1196 CTCCCAGAAGATAACCTCTCCTCGTGGGCCACCTGGGGCACCTTACCACCGGAGCCGAAT 1255	1136 GGGCACCAAGAATCTCTCCCACCACCTGAATTCTCCAAGGACTCGGGTTTCCTGGAAGAG 1195	1076 AGGGCTGGGTCTCTGGCTATTTGGCTGAGAAGGGCCAAGGCCAAGGGCCGGGTGGGGAT 1135	
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              IL28RA splice variant 2
Unpublished
2 (bases 1 to 1476)
Sheppard, P.O., Presnell, S.R., Fox, B.A., Gil
and Grant, P.J.
Direct Submission
Submitted (05-UU-2002) Bioinformatics, Zyr
Bastlake Avenue Bast, Seattle, WA 98102, Ut
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1476 bp mRNA linear PRI 26-NOV-2002
HOmo sapiens interleukin 28 receptor A splice variant 2 (IL28RA)
mRNA, complete cds; alternatively spliced.
                                                                                                                                                             Homo
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                                                                                                             Fox, B.A., Gilbert, T., Haldeman, B.
                ZymoGenetics,
, USA
                                                         Gilbert, T.,
                                                         Haldeman, B.A.
                          Inc.,
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ATCTACACGTTCAGTGTCCCGAAATACAGCAAGTTCTCTAAGCCCACCTGCTTCTTGCTG
                                         CCAGTCCAGATCACTCTCCAGCCAGCTGCCAGGGAACACCACTGCCTCAGTGCCAGAACCC
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                     1476 bp
Sequence 1 from Patent WO0244209
AX473-47
 Presnell, S.R., Xu, W., Novak, J.E., Whitmore, T.E. and Grant, F.J. Cytokine receptor zcytor19
Patent: WO 0244209-A 1 06-JUN-2002;
                                                                                    Homo sapiens (human)
                                                                                                                               AX478497.1
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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PEEEEEARESELEDSDAGSWGAESTQRTSDRGKTLGHYMAR"

09 a 439 c 456 g 272 t
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Pred. No. 5.2e-311;
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                            Presnell, S.R., Xu,W., Novak,J.E., Whitmore,T.B. and Cytokine receptor zcytor19
Patent: WO 0244209-A 3 06-JUN-2002;
ZymoGenetics, Inc. (US)
                                                                   synthetic construct
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Pred. No. 2.2e-209;
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AL Submitted (01-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gj:18125066.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeate; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr:, TREMBL; Mp:, WORMPBP; Information on the WORMPBP http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Further information can be found at http://www.sanger.ac.uk/HOP/Chri
RPI1-10N16 is from the library RPCI-111 constructed by the group of Pieter de Jong. For further details see
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om clone RP11-10N16 on chromosome
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Best Local Similarity
Matches 796; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
VBCTOR: pBACe3.6
VBCTOR: pBACe3.6
This sequence is the entire insert of clone RP11-10N16 The true
left end of clone RP11-509P14 is at 17440 in this sequence. The
true right end of clone RP11-293P20 is at 7865 in this sequence
Location/Qualifiers
                                                                                                                           TCCTCCTGGGCCACCTGGGGCACCTTACCACCGGAGCCGAATCTGGTCCCTGGGGGGACCC 1273
                                                                                                                                                                                             CACCACCIGAATTCTCCAAGGACTCGGGTTTCCTGGAAGAGCTCCCAGAAGATAACCTC
                                                                                                                                                                                                                                                                                                                   TATTTGGCTGAGAAGGGGCCAGGCCAAGGGCCGGGTGGGGATGGGCACCAAGAATCTCTC 1153
                                                                                                                                                                                                                                                                                                                                                                                       TCAGACAGAAGCTGGGCCAGCACTGTGGACTCCTGGGACAGGGCTGGGTCCTCTGGC
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       CAGTTTCTCTTCAGACACTGACCTTCTGCTGGGAAAGCAGCCCTGAGGAAGAAGAGGAG
                                            CCAGTTTCTCTCAGACACTGACCTTCTGCTGGGAAAGCAGCCCTGAGGAGGAAGAGAGGAG 1333
                                                                                                                                                                                                                          CCACCACCTGAATTCTCCAAGGACTCGGGTTTCCTGGAAGAGCTCCCAGAAGATAACCTC 1213
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                                                                                                   TCCTCCTGGGCCACCTGGGGCACCTTACCACCGGAGCCGAATCTGGTCCCTGGGGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11.1"
51656. .51817
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(AL358412). Assembly confirmed by restriction digest."
38933 c 39092 g 44269 t
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Sequence from overlapping clone RP11-509P14 (AL358412). Assembly confirmed by restriction dige
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Pred. No. 2.9e-189
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ACCESSION VERSION KEYWORDS

REFERENCE

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RESULT 10

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Matches 617
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Sequence 22 from Patent WO0244209.
AX478518
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Patent: W 0.244209-A 22 06-JUN-2002;
ZymoGenetics, Inc. (US)
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                                                                                                                                                                                                                                  CTGACATGGCTCCCAGGGCTTGGCAACCCCCAGGATGTGACCTATTTTGTGGCCTATCAG
                                                                                                                                                                                                                                                                              AGGCCCCGTCTGGCCCCCCAGAATGTGACGCTGCTCTCCCAGAACTTCAGCGTGTAC
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                                                   CTATGTTCTATGATGTGCCTGAAGAAACAGGACCTGTACAACAAGTTCAAGGGACGCGTG
                                                                                                          AGCTCTCCCACCCGTAGACGGTGGCGCGAAGTGGAAGAGTGTGCGGGAACCAAGGAGCTG
                                                                                                                                        AGCTCTCCCACCCGTAGACGGTGGCGCGAAGTGGAAGAGTGTGCGGGAACCAAGGAGCTG
                                                                                                                                                                                            CTGACATGGCTCCCAGGGCTTGGCAACCCCCAGGATGTGACCTATTTTGTGGCCTATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trans1 table=1
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/byotein id="CAD4397.1"
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YGLPFCMPBLDLKYEVAFMKEGAGNKTLFPCPCPAFBLAGASSVFLEFPKPKDT
LMISRTPENTCVVTDVSHEDPSVENMYVTDGVSVHNAKTKPREGOYNSTYRVLSVLTV
LHQDMLNGKEYKCKVSNKALPSSIEKTISKAKGOPRBPOVYTLPPSRDELTKNQVSUTTV
LHQDMLNGKEYKCKVSNKALPSSIEKTISKAKGOPRBPOVYTLPPSRDELTKNQVSUTF
CLVKGFYPSDIAVFMESNGOPSNNYKTTPPVLDSDGSFFLYSKLTVDKSRMQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK"
451 c 377 g 263 t
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/note="Zcytor17-Fc4 fusion protein"
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98.9%;
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Pred. No. 1.1e-145;
0; Mismatches 7;
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AUTHORS
TITLE
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ORGANISM
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Patent: WO 0244209-A 32 06-JUN-2002;
ZymoGenetics, Inc. (US)
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Grant, F.J.

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REFERENCE AUTHORS TITLE JOURNAL

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Donnelly,R.P.
IFN-lambdas mediate antiviral p.
II cytokine receptor complex
Nat. Immunol. (2002)
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     2 (bases 1 to 1608)

Kotenko,S.V.

Direct Submission

Submitted (20-NOV-2002) Biochemistry & Molecular Biology,

University of Medicine and Dentistry of New Jersey, New Jersey

Medical School, 185 South Orange Avenue, Newark, NJ 07103, USA
                                                                                                                                                                                                                                                       AY184376 1608 bg
Mus musculus class II cytokine
AY184376 1 GI:27261796
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Mammalia; Eutheria; Rodentia;
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ISGSLSKRDLAVWEPFVSLOTLTFCWVNNPEGEBEQEDEBEBEBEBEBEBBKG
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AY129153 674 bp mRNA linear PRI 26-NOV-2002 Homo sapiens interleukin 28 receptor A splice variant 3 (IL28RA) mRNA, complete cds; alternatively spliced.
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Patent: WO 0244209-A 20 06-JUN-2002;
ZymoGenetics, Inc. (US)
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CCAATGCCACGTACCAGCTGCCCCCTGCATGCCCCCACTGGATCTGAAGTATGAGGTG 486			CGGACGGTTTCTCCCAGCTCCAAGTCCCCCTCGGTGGAGTCCGAATACCTTGAATTACCTT 366	CTATGTTCTATGATGTGCCTGAAGAAACAGACCTGTACAACAAGTTCAAGGGACGCGTG 306	AGCTCTCCCACCGTAGACGGTGGCGCAAGTGGAACAGTTTTCCGGGAACCAAGGAGCTG 246 	TGACATGGCTCCCAGGGCTTGGCAACCCCCAGGATGTGACCTATTTTGTGGCCTATCAG 180	CTGACATGGCTCCCAGGGCTTGGCAACCCCCAGGATGTGACCTATTTTGTGGCCTATCAG 186	AGGCCCGTCTGGCCCTCCCCAGAATGTGACGCTGCTCTCCCAGAACTTCAGCGTGTAC 126	TGGCGGGCCCGAGCGCTGGGCCCCCTGCTCCTGTGCCTGCAGGCCGCTCCAGGG 60	ATGGCGGGGCCCGAGCGCCTGGGGCCCCCTGCTGCTGCTGCAGGCCGCTCCAGGG 66	34.6%; Score 510; DB 9; Length 674; Similarity 100.0%; Pred. No. 2.3e-119; 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/gene="1128RA" /note="alternatively spliced" /codon_start=1 /codon_start=1 /product_"interleukin 28 receptor A splice variant 3" /protein_id="AAN28268.1" /protein_id="AAN28268.1" /db_xxef="GI:55527136" /translation="MAGDERWGELLCLIQAAPGRERLAEPDONVTLLSONFSVYLTWL PGLGNPQDVTYFVAYQSSFTRRKWERDECAGTKELLCSANGTCKKGDLYKKFKGRVRT VSPSSKSPWYESTLDYLEFVEPAPPVLVTQTEBILSANGTYQLEPGVPPLDLKYEV AFWKEGAGNKVGSSFPAPRLGPLLHPFLLRFFSPSQPAPAPLLQEVFPVHS" 128 a 223 c 182 g 141 t	/gene="luzeka" /note="synonym: zcytor19" 1636		/organism="Homo saniens"	venue East, Seattle, WA 9 ocation/Qualifiers	informatics,	IL28RA splice variant 3 Unpublished 2 (bases 1 to 674) Sheppard,P.O., Presnell,S.R., Fox,B.A., Gilbert,T., Haldeman,B.A.	to 674) O., Presnell,S.R., Fox,B.A., Gilbert,T., F	sapiens (human) sapiens ryota; Metazos; Chordata; Craniata; Vertebrata; alia; Eutheria: Primates: Catarrhin; Hominidae

Search completed: September 17, 2003, 20:57:17 Job time : 3634.68 secs